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[illegible]

# FIG. 1B

657	666	675	684	693	702
TCC AAT ATC CTT TCC	CAT TCC TAC TGC	CTA CAC CAA GAT	GTC ATG AAG CTG	GCC	
S N I L S	H S Y C L	H Q D V	M K L	A	
711	720	729	738	747	756
TGT GAT GAT ATC CGG	GTC AAT GTC	GTC TAT GGC	CTT ATC GTC	ATC ATC TCC	GCC
C D D I R	V N V V	Y G L	I V I I S	A	
765	774	783	792	801	810
ATT GGC CTG GAC TCA	CTT CTC ATC	TCC TTC TCA	TAT CTG CTT	ATT CTT AAG	ACT
I G L D S	L L I S F	S Y L L I	L K	T	
819	828	837	846	855	864
GTG TTG GGC TTG ACA	CGT GAA GCC	CAG GCC AAG	GCA TTT GGC	ACT TGC	GTC TCT
V L G L T R	E A Q A K	A	F G T C V	S	
873	882	891	900	909	918
CAT GTG TGT GCT GTG	TTC ATA TTC	TAT GTA CCT	TTC ATT GGA	TTG TCC	ATG GTG
H V C A V F	I F Y V P	F I G L S	M	V	
927	936	945	954	963	972
CAT CGC TTT AGC AAG	CGG CGT GAC	TCT CCG CTG	CCC GTC ATC	TTG GCC	AAT ATC
H R F S K R	R D S P	L P V I L	A N I		
981	990	999	1008	1017	1026
TAT CTG CTG GTT CCT	CCT GTG CTC	AAC CCA ATT	GTC TAT GGA	GTG AAG	ACA AAG
Y L L V P P	V L N P I	V Y G V	K T K		
1035	1044	1053	1062	1071	1080
GAG ATT CGA CAG CGC	ATC CTT CGA	CTT TTC CAT	GTG GCC	ACA CAC	GCT TCA GAG
E I R Q R I	L R L F	H V A T	H A S	E	
1089	1098	1107	1116	1125	1134
CCC TAG GTG TCA GTG	ATC AAA CTT	CTT TTC CAT	TCA GAG	TCC TCT	GAT TCA GAT
P *					
1143	1152	1161	1170	1179	1188
TTT AAT GTT AAC ATT	TTG GAA GAC	AGT ATT CAG	AAA AAA AAT	TTC CTT	AAT AAA
1197	1206	1215	1224	1233	1242
AAA TAC AAC TCA GAT	CCT TCA AAT	ATG AAA CTG	GTT GGG GAA	TCT CCA	TTT TTT
1251	1260	1269	1278	1287	1296
CAA TAT TAT TTT CTT	CTT TGT TTT	CTT GCT	ACA TAT AAT	TAT TAA	TAC CCT GAC
1305	1314	1323	1332	1341	1350
TAG GTT GTG GTT GGA	GGG TTA TTA	CTT TTC ATT	TTA CCA	TGC AGT	CCA AAT CTA

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1

2385			2394			2403			2412			2421			2430		
CTT	CTG	AGG	GGC	TAT	TAC	CAA	GGG	TTA	ATA	GGT	TTC	ATC	TTC	AAC	AGG	ATA	
2439			2448			2457			2466			2475			2484		
CAA	CAG	TGT	TAA	CCA	AGA	AAC	TCA	AAT	TAC	AAA	TAC	TAA	AAC	ATG	TGA	TCA	
2493			2502			2511			2520			2529			2538		
ATG	TGG	TAA	GTT	TCA	TTT	TCT	TTT	TCA	ATC	CTC	AGG	TTC	CCT	GAT	ATG	GAT	
2547			2556			2565			2574			2583			2592		
TAT	AAC	ATG	CTT	TCA	TCC	CCT	TTT	GTA	ATG	GAT	ATC	ATA	TTT	GGA	AAT	GCC	
2601			2610			2619			2628			2637			2646		
TTA	ATA	CTT	GTA	TTT	GCT	GCT	GGA	CTG	TAA	GCC	CAT	GAG	GGC	ACT	GTT	TAT	
2655			2664			2673			2682			2691			2700		
TGA	ATG	TCA	TCT	CTG	TTC	ATC	ATT	GAC	TGC	TCT	TTG	CTC	ATC	ATT	GAA	TCC	
2709			2718			2727			2736			2745			2754		
AGC	AAA	GTG	CCT	AGA	ACA	TAA	TAG	TGC	TTA	TGC	TTG	ACA	CCG	GTT	ATT	TTT	
2763			2772			2781			2790			2799			2808		
CAA	ACC	TGA	TTC	CTT	CTG	TCC	TGA	ACA	CAT	AGC	CAG	GCA	ATT	TTC	CAG	CCT	
2817			2826			2835			2844			2853			2862		
TTG	AGT	TGG	GTA	TTA	TTA	AAT	TCT	GGC	CAT	TAC	TTC	CAA	TGT	GAG	TGG	AAG	
2871			2880			2889			2898			2907			2916		
CAT	GTG	CAA	TTT	CTA	TAC	CTG	GCT	CAT	AAA	ACC	CTC	CCA	TGT	GCA	GCC	TTT	
2925			2934			2943			2952			2961			2970		
GTT	GAC	ATT	AAA	TGT	GAC	TTG	GGA	AGC	TAT	GTG	TTA	CAC	AGA	GTA	AAT	CAC	
2979			2988			2997			3006			3015			3024		
AAG	CCT	GGA	TTT	CTG	AAA	AAA	CTG	TGC	AGA	GCC	AAA	CCT	CTG	TCA	TTT	GCA	
3033			3042			3051			3060			3069			3078		
CCC	ACT	TGT	ATT	TGT	ACG	AGG	CAG	TTG	GAT	AAG	TGA	AAA	ATA	AAG	TAC	TAT	
3087			3096			3105			3114			3123			3132		
GTC	AAG	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	AAA	

AAA A 3'

FIG. 2

1	15 16	30 31	45 46	60 61	75 76	90	
1	101P3A11	MMVDPNNESSATYF	ILIGLPGLEEAQFWL	APPLCSLYLIAVLGN	LTIYIVRTEHSIHE	PMYIFLCMLSGIDIL	ISTSSMPKMLAIFWF 90
2	RALC	-MSSCN---FTHATF	MLIGIPGLEEAHFWF	GPPLLSMYAVALEGN	CIWVFIVRTERSLSHA	PHYLFLCMLAAIDLA	LSTSTMPKILALFWF 86
3	HPRAJ70	-MSSCN---FTHATC	VLIGIPGLEKAHFWV	GPPLLSMYVAMCGN	CIWVFIVRTERSLSHA	PHYLFLCMLAAIDLA	LSTSTMPKILALFWF 86
	91	105 106	120 121	135 136	150 151	165 166	180
1	101P3A11	NSTTIQFDACLLQIF	AIHSLSGMESTVLLA	MAFDRYVAICHPLRH	ATVLTLPRTVKIGVA	AVVRGAALMAPLPVF	IKQLPFCRSNILSHS 180
2	RALC	DSREITFDACLAQMF	FIHALSAIESTILLA	MAFDRYVAICHPLRH	AAVLNNTVTQIGHV	ALVRGSLPFFPLPLL	IKRLAFCHSNVLSHS 176
3	HPRAJ70	DSREISIEACLTQMF	FIHALSAIESTILLA	MAFDRYVAICHPLRH	AAVLNNTVTAQIGIV	AVVRGSLPFFPLPLL	IKRLAFCHSNVLSHS 176
	181	195 196	210 211	225 226	240 241	255 256	270
1	101P3A11	YCLHQDVMKLCACDDI	RVNWVYGLVITISAI	GLDSLISFSYLLIL	KTVLGLT-REAQAKA	FGTCVSHVCNVFIYF	VPTIGLSMVHRESKR 269
2	RALC	YCVHQDVMKLAYTDT	LPNVVYGLTAILLYM	GVDVMFISLSYFLII	RAVLQLPSKSERAKA	FGTCVSHIGVVLAFY	VPLIGLSVVHRRFGNS 266
3	HPRAJ70	YCVHQDVMKLAYADT	LPNVVYGLTAILLYM	GVDVMFISLSYFLII	RTVLQLPSKSERAKA	FGTCVSHIGVVLAFY	VPLIGLSVVHRRFGNS 266
	271	285 286	300 301	315 316	330 331	345 346	360
1	101P3A11	RDSPLPVILANIYLL	VPPVLNPIVYGKTK	EIRQIRILRPHVATH	ASEP-----		
2	RALC	LDPFIVHVMGDVYLL	LPPVINPIYGAKTK	QIRTRVLAMFKISCD	KDIEAGGNT	320	
3	HPRAJ70	LHPFIVRVMGDIYLL	LPPVINPIYGAKTK	QIRTRVLAMFKISCD	KDLQAVGGK	320	

FIG. 3

GATCAAACCTCTTTCCATTGAGAGTCCTCTGATTGAGATTTTAATGTAAACATTTTGGAAGACAGTATTCAGAAAAA  
AATTCCTTAATAAAAAATACAACCTGAGATCCTTCAAATATGAACTGGTTGGGGAATCTCCATTTTCAATATTATT  
TCTTCTTTGTTTTCTTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTA  
CCATGCAGTCCAAATCTAACTGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATT  
TGCCAAAGGCCTAAGCACAGCAAAGGAAAATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAACTATAACT  
TCCTCTTTAGAACTCCCAACCACATTTGGATC

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FIG. 4

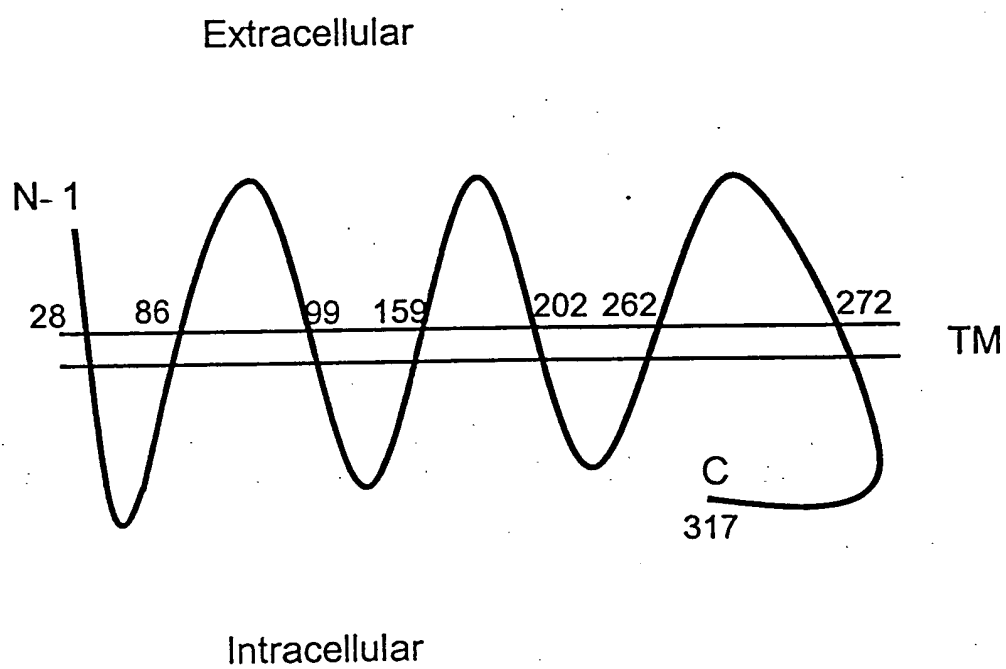




FIG. 5A

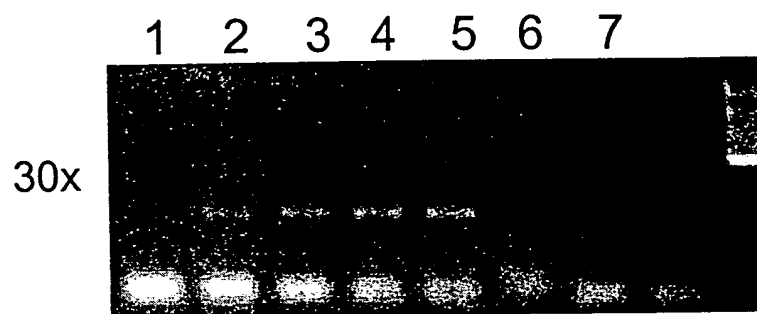


FIG. 5B

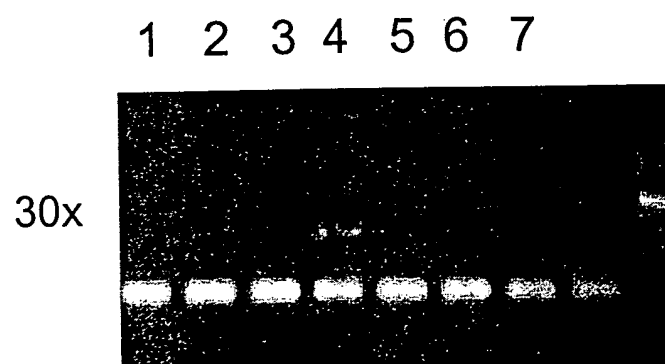


FIG. 6A

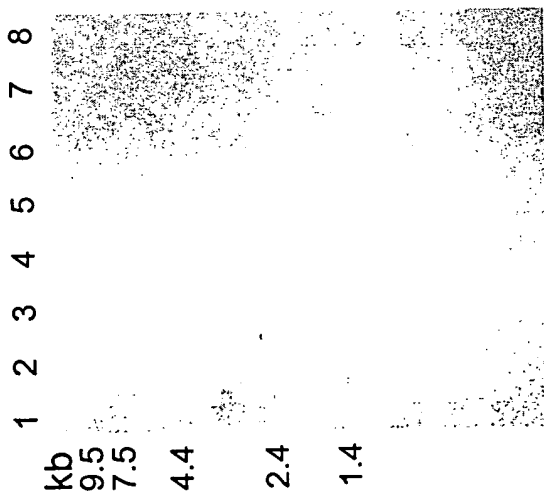


FIG. 6B

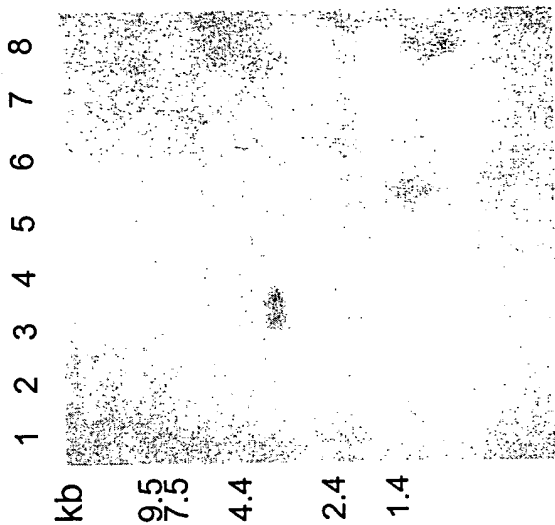
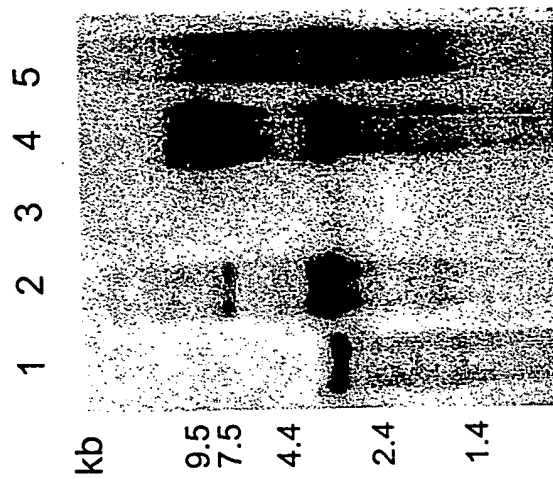


FIG. 6C



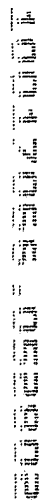


FIG. 8A

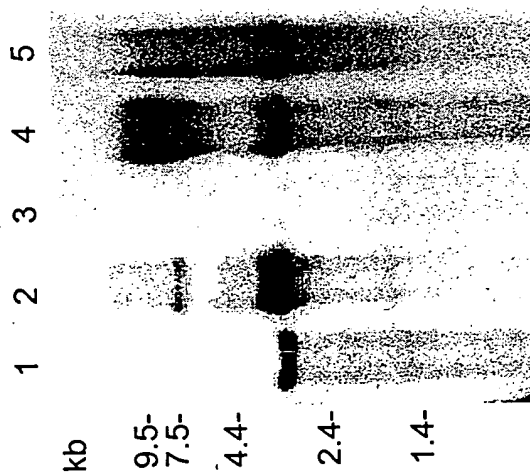


FIG. 8B

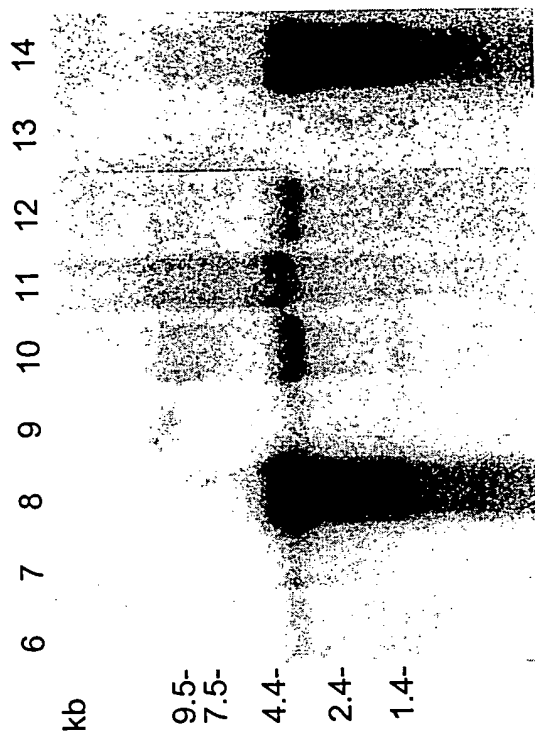
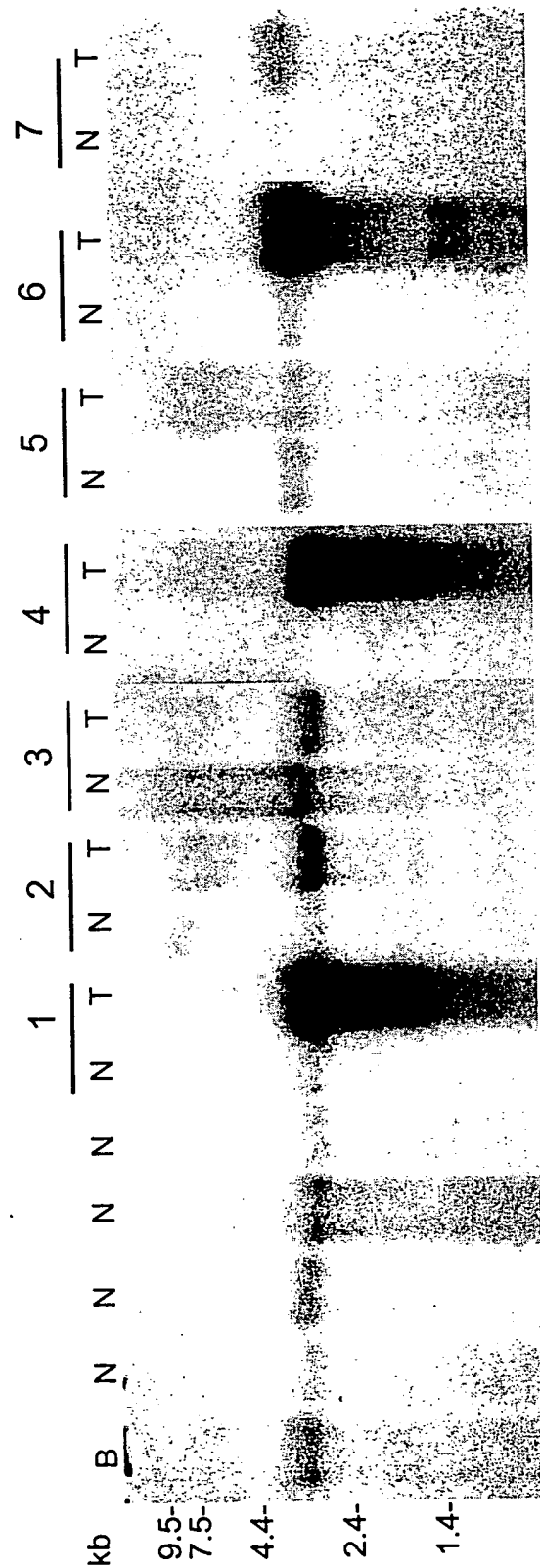


Figure 9A



8 9 10

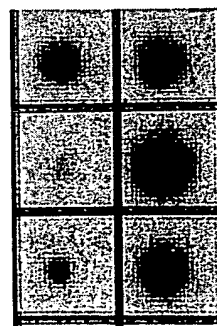


Figure 9B

Figure 10

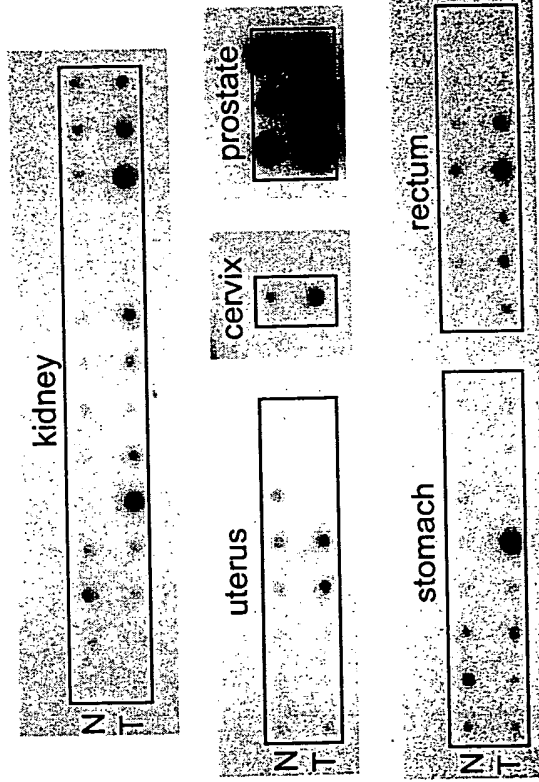
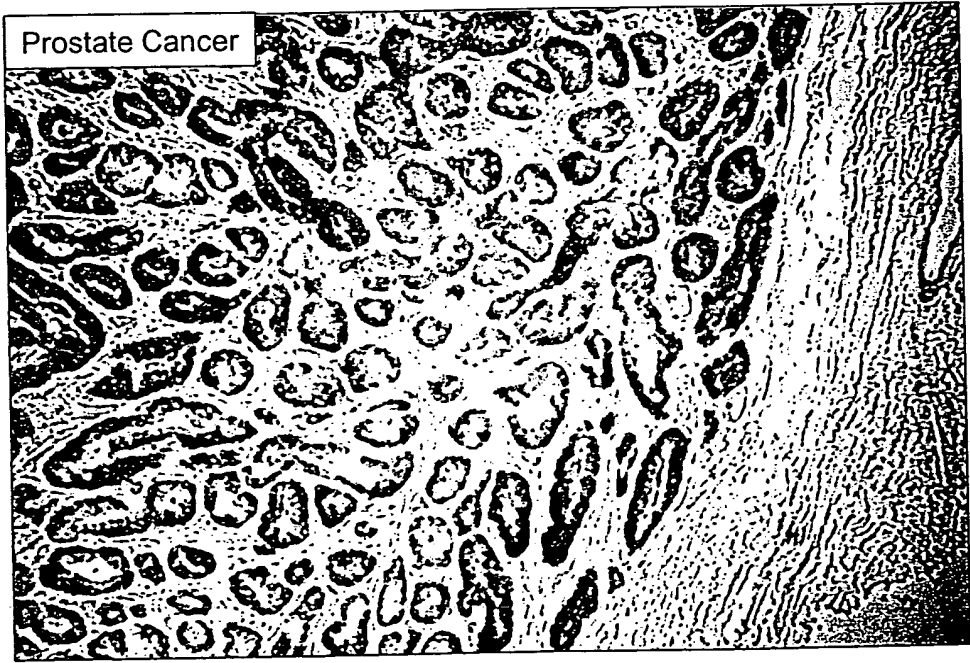


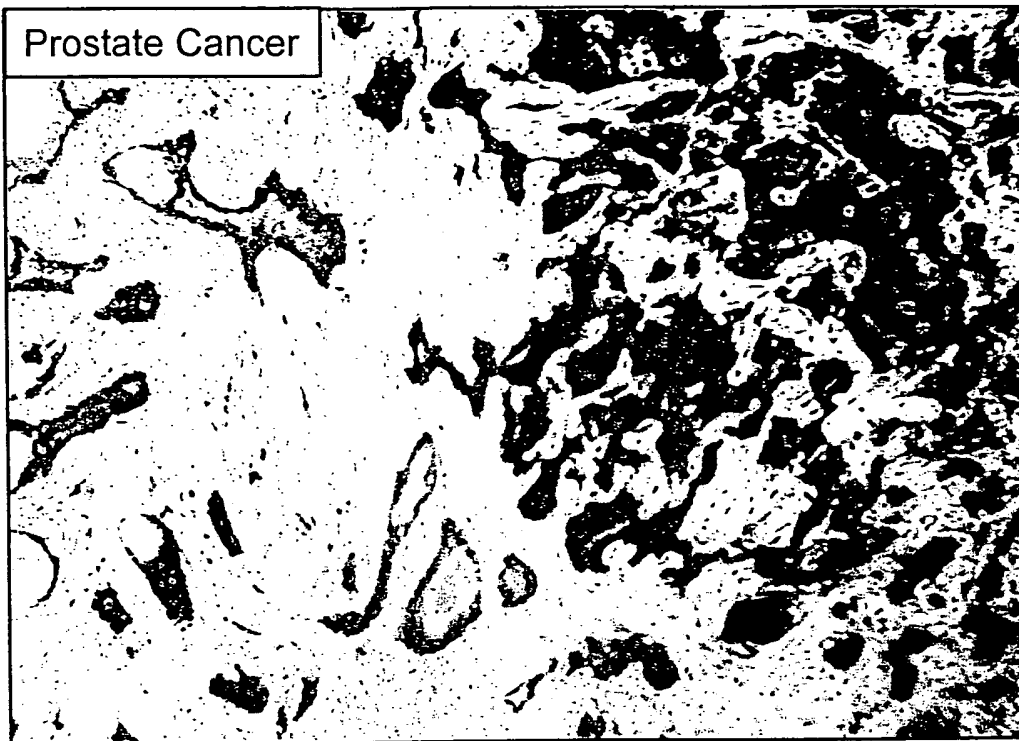
Figure 11A-11B



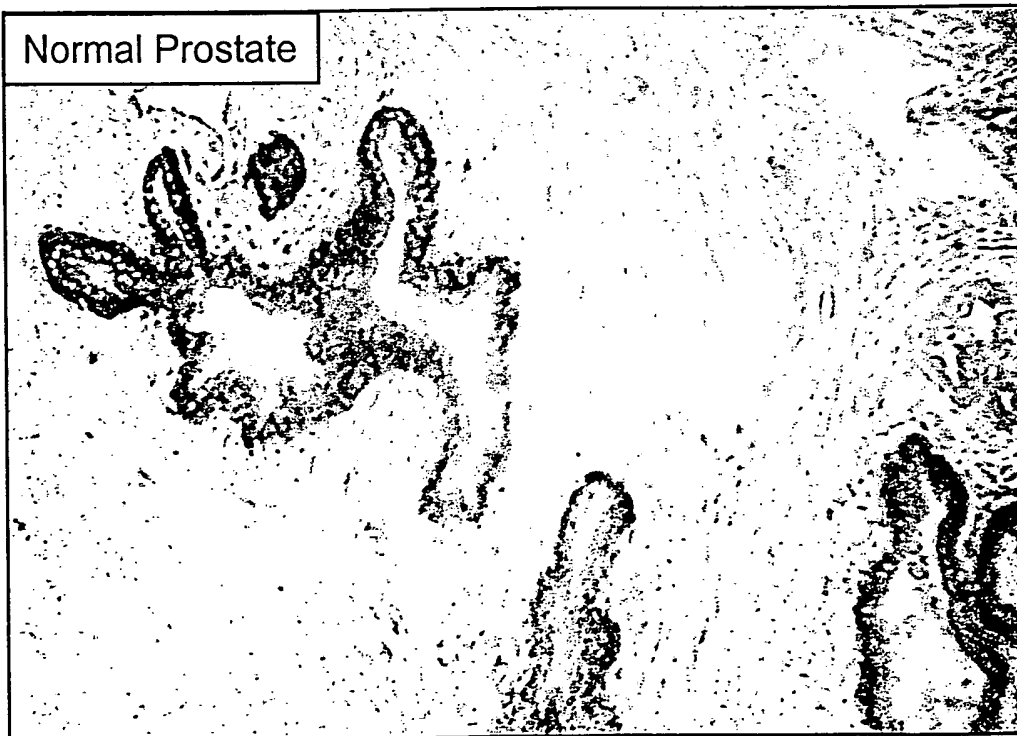
2025035021001

Figure 12A-12B

Prostate Cancer



Normal Prostate



20250530-55024006



FIG. 13A

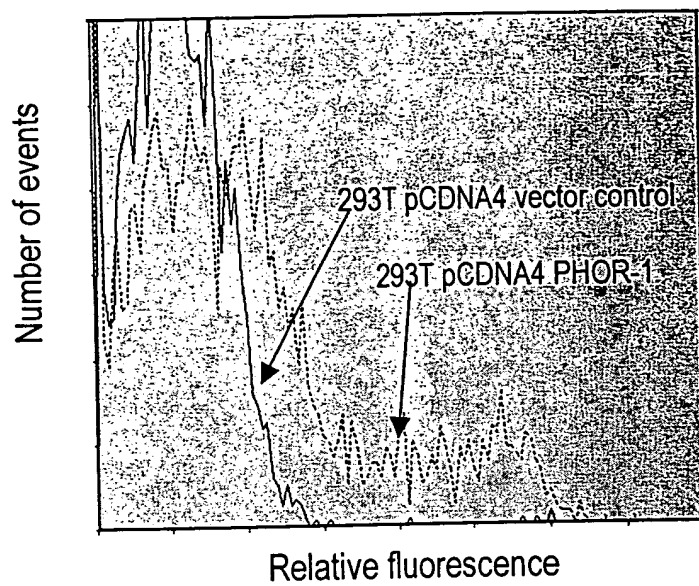


FIG. 13B

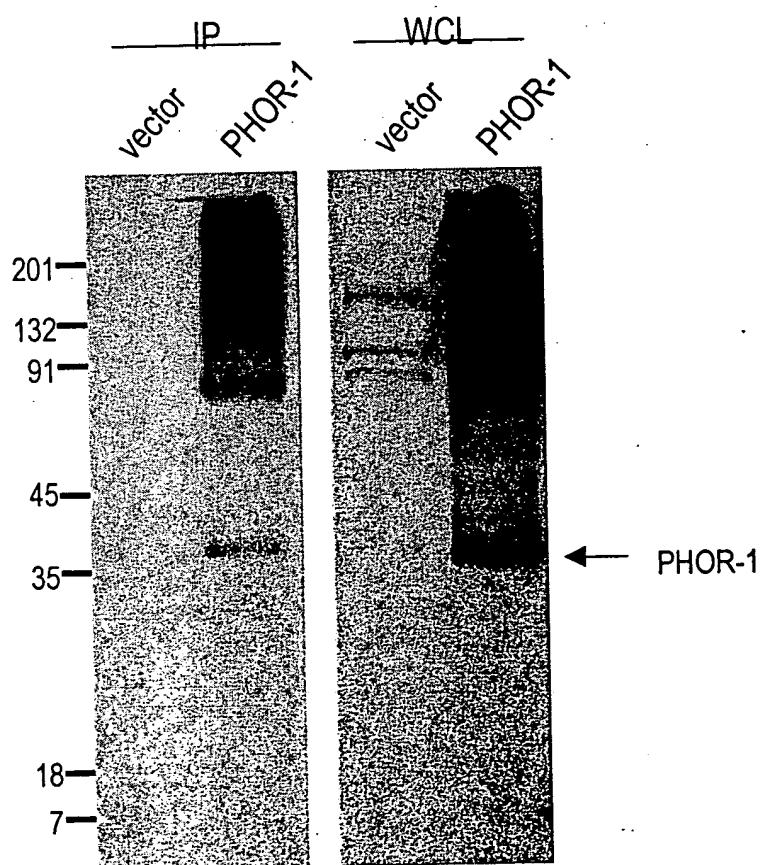


Fig. 14A

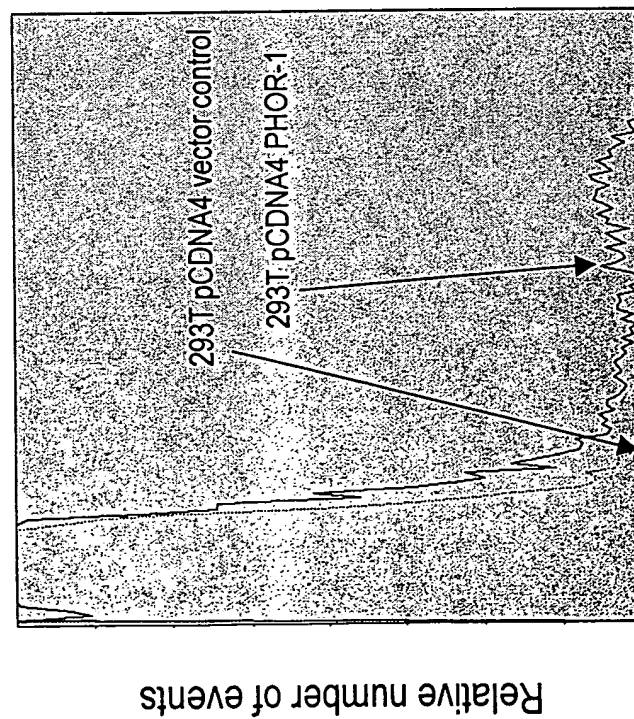
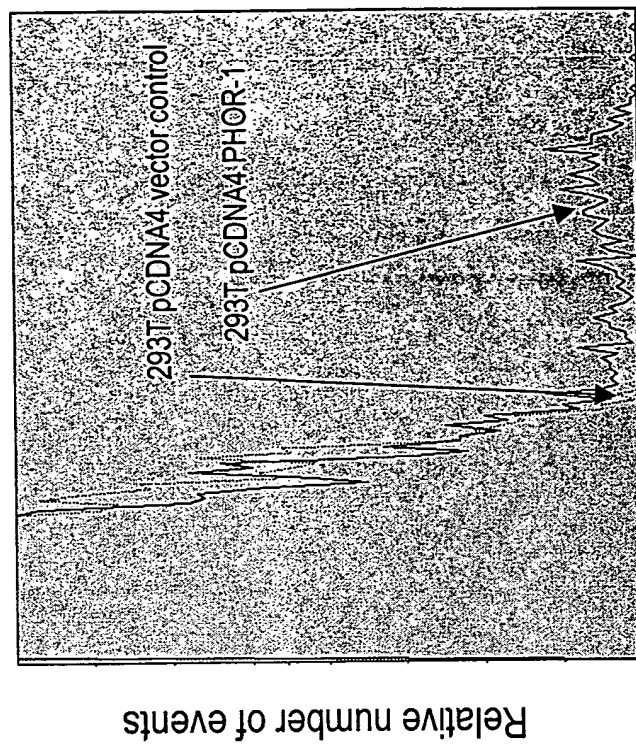


Fig. 14B



Relative fluorescence

Relative fluorescence

Fig. 15

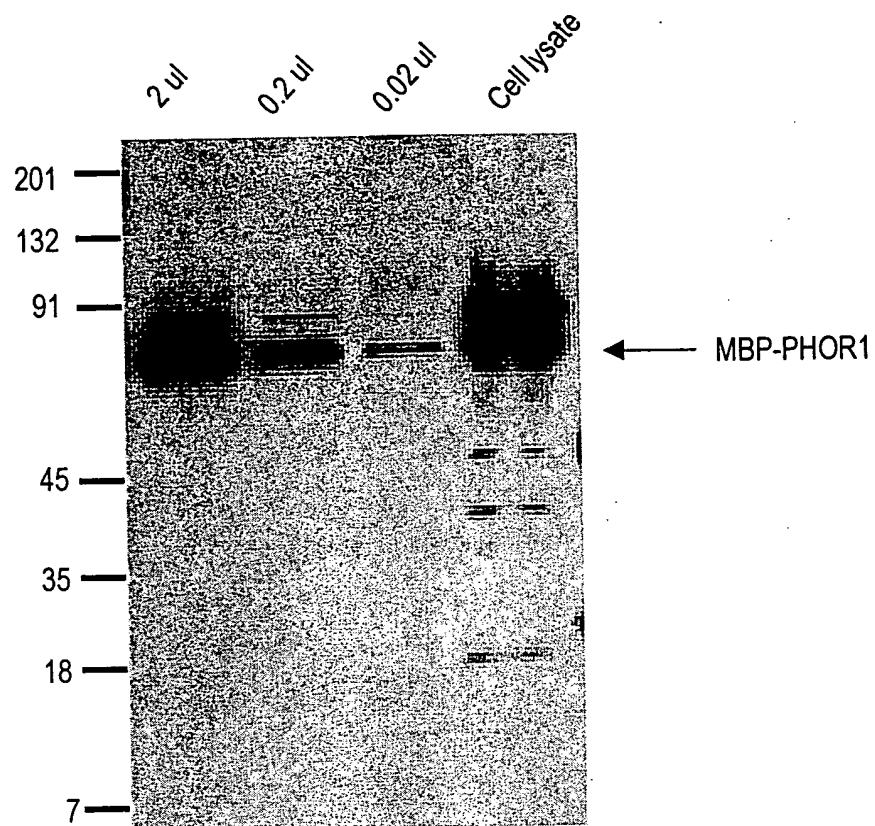


Fig. 16A

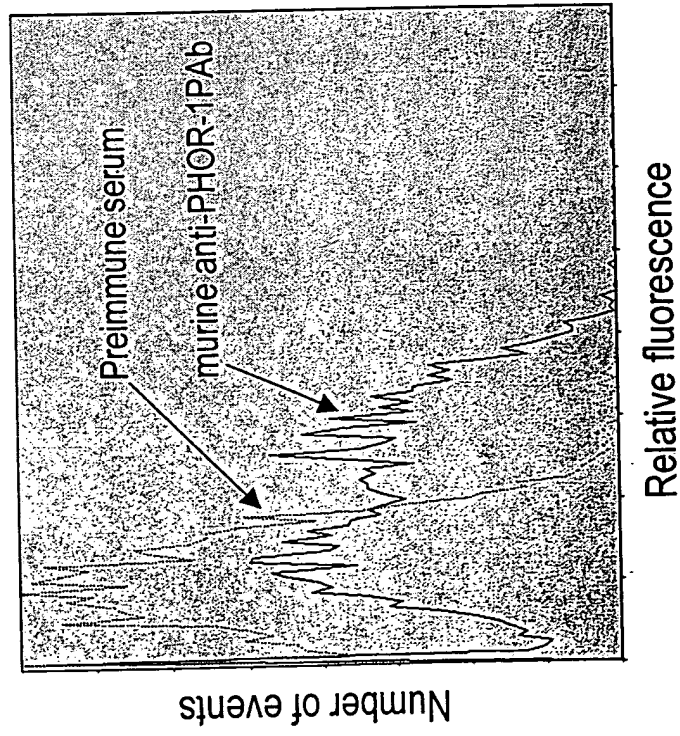
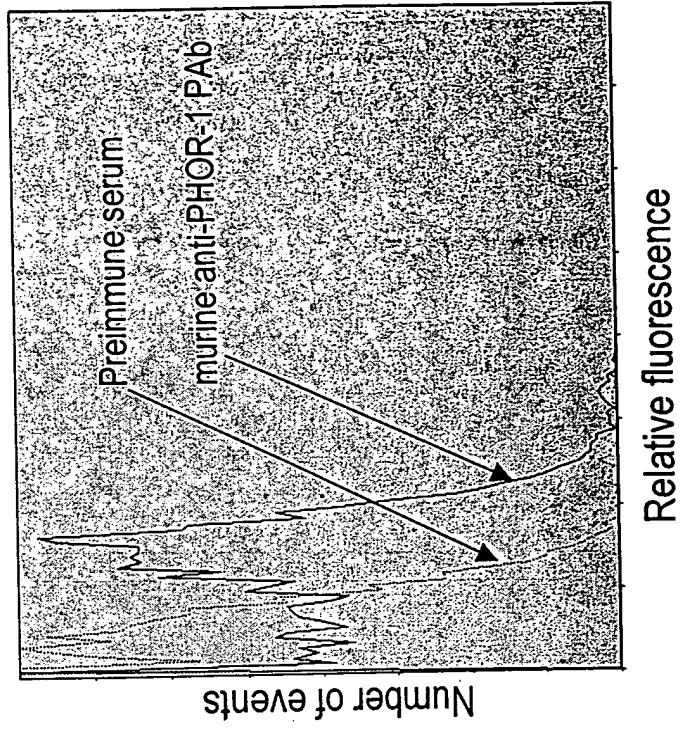


Fig. 16B



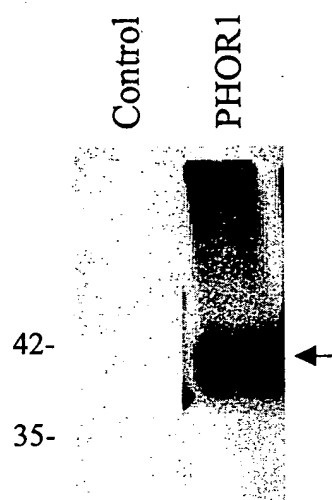


FIG. 17

Figure 18A-F

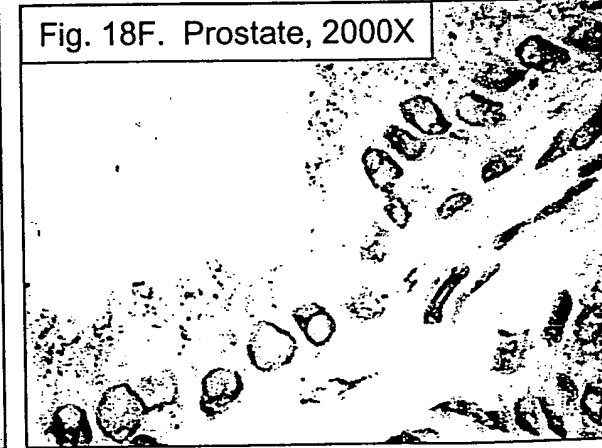
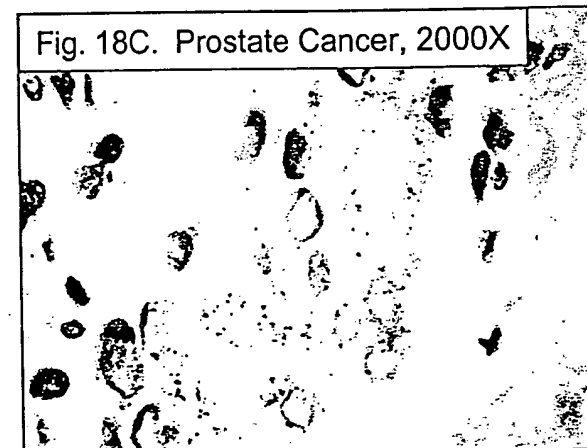
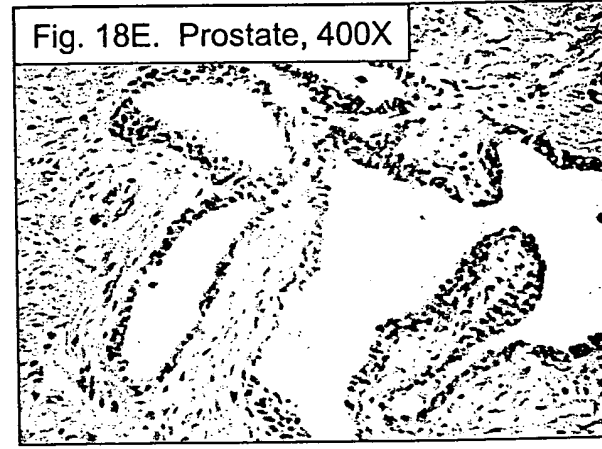
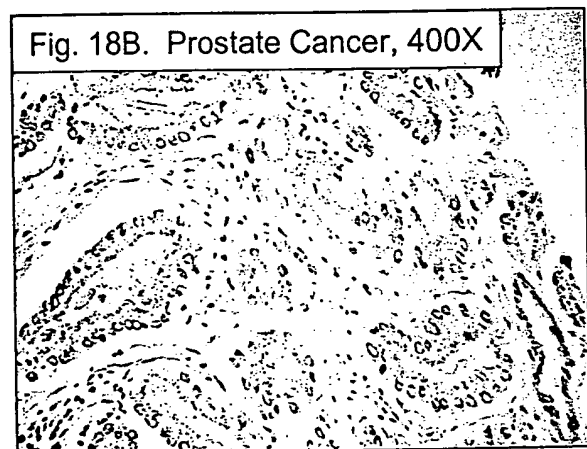
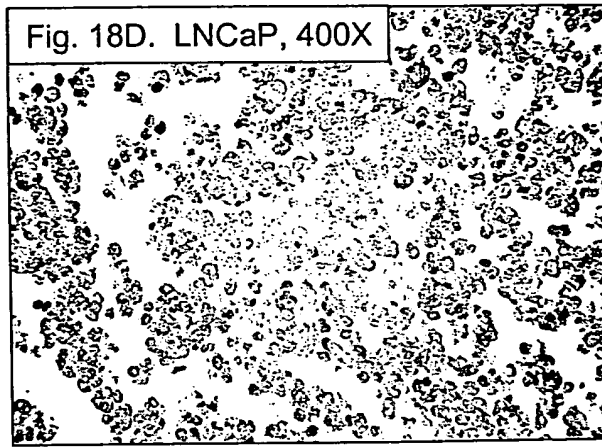
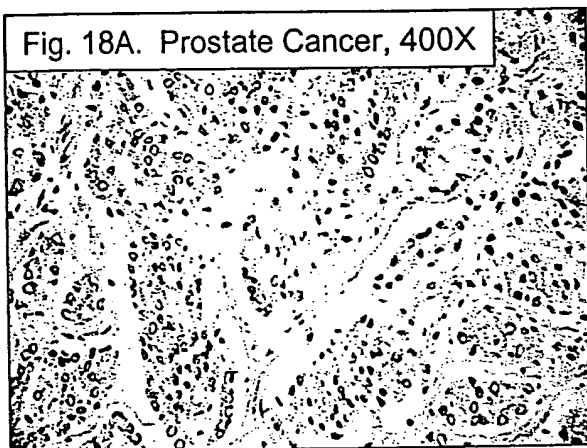


Figure 19A-F

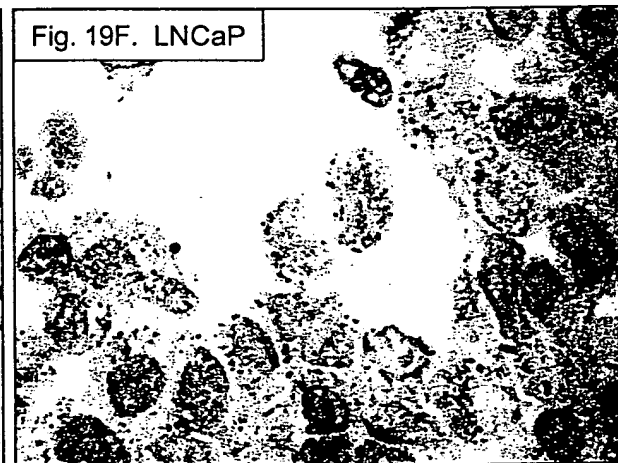
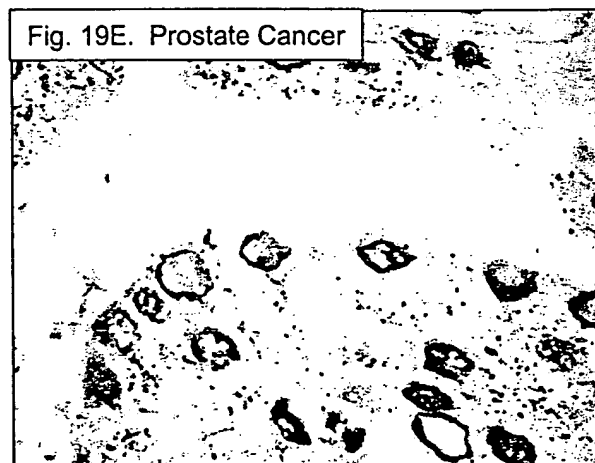
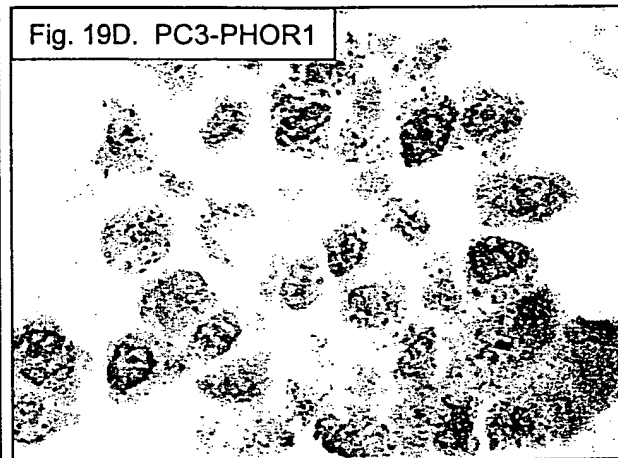
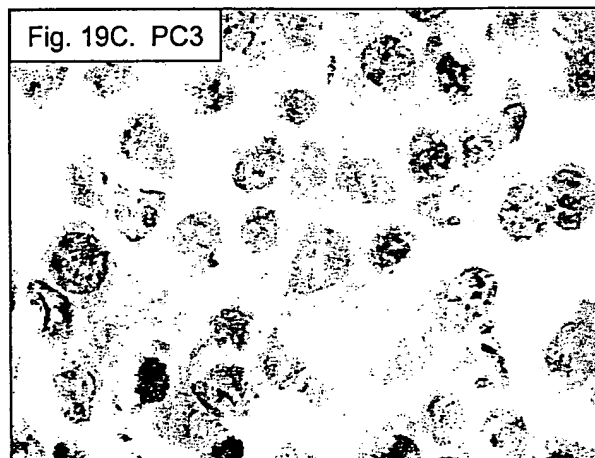
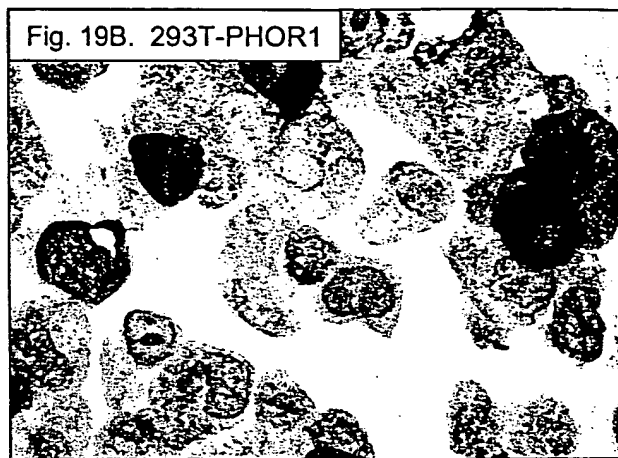
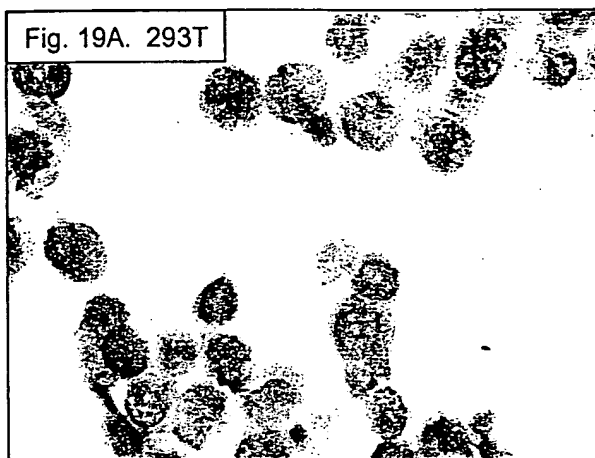
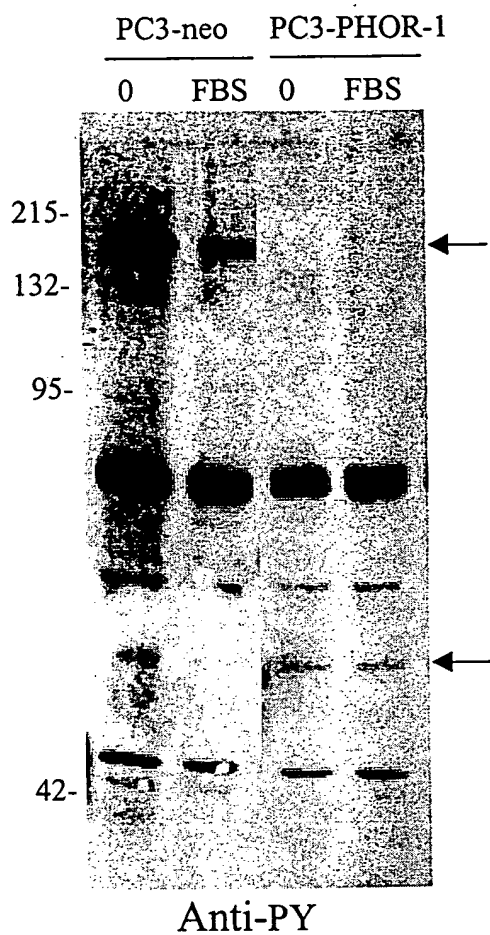
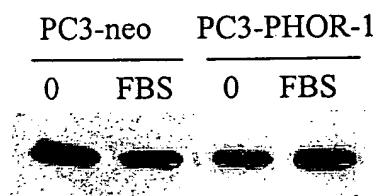


FIG. 20A



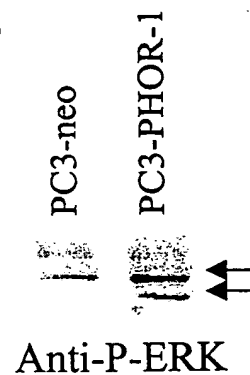
Anti-PY



Anti-Grb2

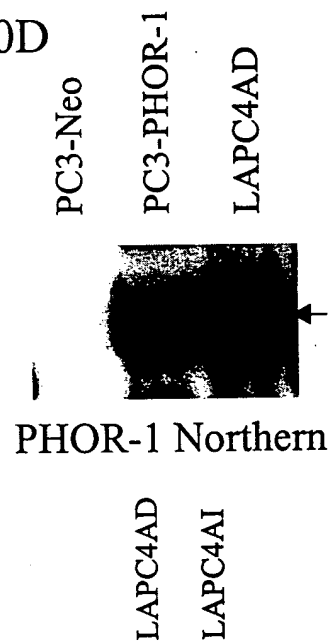
FIG. 20C

FIG. 20B



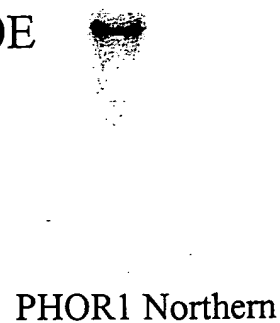
Anti-P-ERK

FIG. 20D



PHOR-1 Northern

FIG. 20E



PHOR1 Northern



Neo



Fig. 21A

20250-99021004

200507 5502700F

PHOR1

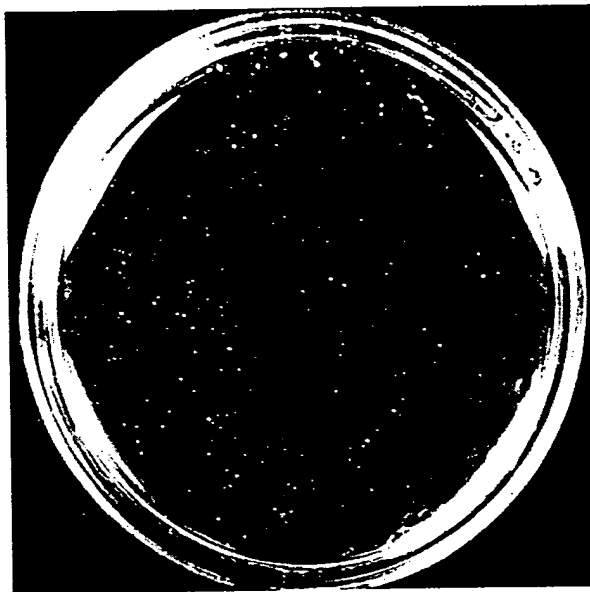


Fig. 21B

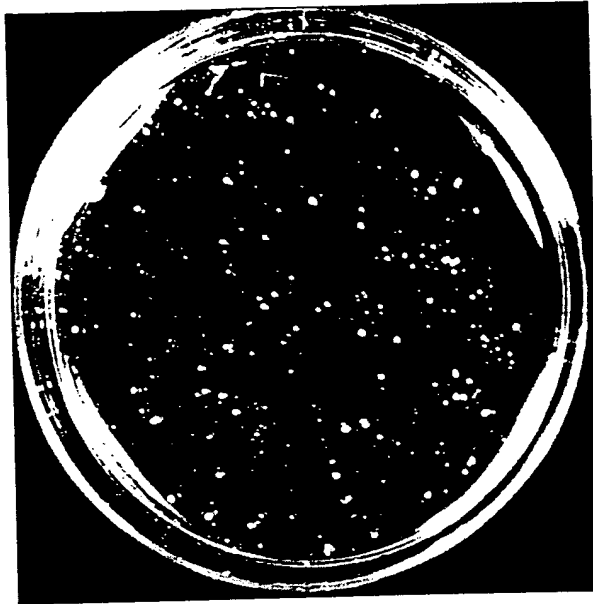


Fig. 21C

[illegible]

FIG. 22

5'		9		18		27		36		45		54						
	GCT	GTG	GCC	ATG	TTT	ATT	GGA	GTG	TTG	GAT	CTA	TTC	TTT	ATC	ATC	CTA	TCT	TAT
	A	V	A	M	F	I	G	V	L	D	L	F	F	I	I	L	S	Y
		63		72		81		90		99		108						
	ATC	TTT	ATC	CTT	CAG	GCA	GTT	CTA	CAA	CTC	TCC	TCT	CAG	GAG	GCC	CGC	TAC	AAA
	I	F	I	L	Q	A	V	L	Q	L	S	S	Q	E	A	R	Y	K
		117		126		135		144		153		162						
	GCA	TTT	GGG	ACA	TGT	GTC	TCT	CAC	ATA	GGT	GCC	ATC	TTA	GCC	TTT	TAC	ACA	CCT
	A	F	G	T	C	V	S	H	I	G	A	I	L	A	F	Y	T	P
		171		180		189		198		207		216						
	TCA	GTC	ATC	TCT	TCA	GTC	ATG	CAC	CGT	GTG	GCC	CGC	TGT	GCT	GTG	CCA	CAC	GTC
	S	V	I	S	S	V	M	H	R	V	A	R	C	A	V	P	H	V
		225		234		243		252		261		270						
	CAC	ATT	CTC	CTC	GCC	AAT	TTC	TAT	CTG	CTC	TTC	CCA	CCC	ATG	GTC	AAT	CCC	ATC
	H	I	L	L	A	N	F	Y	L	L	F	P	P	M	V	N	P	I
		279		288		297		306		315		324						
	ATC	TAT	GGC	GTT	AAG	ACC	AAG	CAG	ATC	CGT	GAC	AGT	CTT	GGG	AGT	ATT	CCT	GAG
	I	Y	G	V	K	T	K	Q	I	R	D	S	L	G	S	I	P	E
		333		342		351		360		369		378						
	AAA	GGA	TGT	GTG	AAT	AGA	GAG	TGA	GGA	ATA	AGT	GGA	AAA	AGA	GTG	GGG	CCC	AGT
	K	G	C	V	N	R	E	*										
		387		396		405		414		423		432						
	GAA	TGC	TGT	AGT	GGG	CCA	GGG	CTG	TGC	TGA	GAG	TAG	ATG	GGT	CCT	AGA	CTC	CAC
		441		450		459		468		477		486						
	GTT	TAG	TTC	TTT	TCT	TGT	ATT	ATG	AAA	AGA	ATA	AAT	GAT	GTC	CTG	AAG	CTC	AGA
		495																
	AAA	AAA	AAA	AAA	AAA	3'												

5'-GGG-3'